



SEQUENCE LISTING

<110> O'Brien, John S.

<120> METHODS FOR ALLEVIATING NEUROPATHIC PAIN

<130> 07256/024001

<140> 08/928,074

<141> 1997-09-11

<150> 08/611,307

<151> 1996-03-05

<150> PCT/US97/04143

<151> 1996-03-05

<160> 25

<170> PatentIn Ver. 2.0

<210> 1

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
peptide sequence

<400> 1

Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys  
1 5 10 15

Thr Glu Lys Glu Ile Leu  
20

<210> 2

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<220>

<221> MOD\_RES

<222> (2)

<223> Ala at position 2 is a D-enantiomer

<400> 2

Thr Ala Leu Ile Asp Asn Asn Ala Thr Glu Glu Ile Leu Tyr  
1 5 10

<210> 3  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Artificial Peptide Sequence (Amino acids 18-29 of  
saposin C)

<400> 3  
Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu  
1 5 10

<210> 4  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Mouse)

<400> 4  
Cys Gln Phe Val Met Asn Lys Phe Ser Glu Leu Ile Val Asn Asn Ala  
1 5 10 15

Thr Glu Glu Leu Leu Tyr  
20

<210> 5  
<211> 21  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Rat)

<400> 5  
Cys Gln Leu Val Asn Arg Lys Leu Ser Glu Leu Ile Ile Asn Asn Ala  
1 5 10 15

Thr Glu Glu Leu Leu  
20

<210> 6

<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Guinea Pig)

<400> 6  
Cys Glu Tyr Val Val Lys Lys Val Met Leu Leu Ile Asp Asn Asn Arg  
1 5 10 15

Thr Glu Glu Lys Ile Ile  
20

<210> 7  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (Bovine)

<400> 7  
Cys Glu Phe Val Val Lys Glu Val Ala Lys Leu Ile Asp Asn Asn Arg  
1 5 10 15

Thr Glu Glu Glu Ile Leu  
20

<210> 8  
<211> 22  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 8  
Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asp Asn Lys  
1 5 10 15

Thr Glu Lys Glu Ile Leu  
20

<210> 9  
<211> 14  
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 9

Thr Lys Leu Ile Asp Asn Asp Lys Thr Glu Lys Glu Ile Leu  
1 5 10

<210> 10

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 10

Thr Lys Ser Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu  
1 5 10

<210> 11

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hCNTF)

<400> 11

Tyr Val Lys His Gln Gly Leu Asn Lys Asn Ile Asn Leu Asp Ser Val  
1 5 10 15

Asp Gly Val Pro  
20

<210> 12

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-6)

<400> 12

Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Gly

1

5

10

15

<210> 13  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-2)

<400> 13  
Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu  
1 5 10 15

Thr

<210> 14  
<211> 12  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-3)

<400> 14  
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu  
1 5 10

<210> 15  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL1-gamma)

<400> 15  
Phe Tyr Leu Arg Asn Asn Gln Leu Val Ala Gly Thr Leu  
1 5 10

<210> 16  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hEPO)

<400> 16  
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
1 5 10 15

Val

<210> 17  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<400> 17  
Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys  
1 5 10 15

Ala Pro

<210> 18  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hIL-1beta)

<400> 18  
Phe Asn Lys Ile Glu Ile Asn Asn Lys Leu Glu Phe Glu Ser Ala  
1 5 10 15

<210> 19  
<211> 17  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificial  
Peptide Sequence (hONC-M)

<400> 19

Arg Pro Asn Ile Gly Leu Arg Asn Asn Ile Tyr Cys Met Ala Gln Leu  
 1 5 10 15

Leu

<210> 20  
 <211> 18  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificial  
 Peptide Sequence

<400> 20  
 Tyr Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu  
 1 5 10 15

Ile Leu

<210> 21  
 <211> 66  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificial  
 Nucleic Acid Sequence

<220>  
 <221> CDS  
 <222> (1)..(66)

<400> 21  
 tgt gaa ttc ctg gtg aag gag gtg acc aag ctg att gac aac aac aag 48  
 Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys  
 1 5 10 15

act gag aaa gaa ata ctc 66  
 Thr Glu Lys Glu Ile Leu  
 20

<210> 22  
 <211> 2749  
 <212> DNA  
 <213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (1572)

<400> 22

atg tac gcc ctc ttc ctc ctg gcc agc ctc ctg ggc gcg gct cta gcc	48
Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala	
1 5 10 15	
ggc ccg gtc ctt gga ctg aaa gaa tgc acc agg ggc tcg gca gtg tgg	96
Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp	
20 25 30	
tgc cag aat gtg aag acg gcg tcc gac tgc ggg gca gtg aag cac tgc	144
Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys	
35 40 45	
ctg cag acc gtt tgg aac aag cca aca gtg aaa tcc ctt ccc tgc gac	192
Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp	
50 55 60	
ata tgc aaa gac gtt gtc acc gca gct ggt gat atg ctg aag gac aat	240
Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn	
65 70 75 80	
gcc act gag gag gag atc ctt gtt tac ttg gag aag acc tgt gac tgg	288
Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp	
85 90 95	
ctt ccg aaa ccg aac atg tct gct tca tgc aag gag ata gtg gac tcc	336
Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser	
100 105 110	
tac ctc cct gtc atc ctg gac atc att aaa gga gaa atg agc cgt cct	384
Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro	
115 120 125	
ggg gag gtg tgc tct gct ctc aac ctc tgc gag tct ctc cag aag cac	432
Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His	
130 135 140	
cta gca gag ctg aat cac cag aag cag ctg gag tcc aat aag atc cca	480
Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro	
145 150 155 160	
gag ctg gac atg act gag gtg gtg gcc ccc ttc atg gcc aac atc cct	528
Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro	
165 170 175	
ctc ctc ctc tac cct cag gac ggc ccc cgc agc aag ccc cag cca aag	576
Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys	
180 185 190	
gat aat ggg gac gtt tgc cag gac tgc att cag atg gtg act gac atc	624



Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile	
195	200 205
cag act gct gta cgg acc aac tcc acc ttt gtc cag gcc ttg gtg gaa	672
Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu	
210 215 220	
cat gtc aag gag gag tgt gac cgc ctg ggc cct ggc atg gcc gac ata	720
His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile	
225 230 235 240	
tgc aag aac tat atc agc cag tat tct gaa att gct atc cag atg atg	768
Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met	
245 250 255	
atg cac atg caa ccc aag gag atc tgt gcg ctg gtt ggg ttc tgt gat	816
Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp	
260 265 270	
gag gtg aaa gag atg ccc atg cag act ctg gtc ccc gcc aaa gtg gcc	864
Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala	
275 280 285	
tcc aag aat gtc atc cct gcc ctg gaa ctg gtg gag ccc att aag aag	912
Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys	
290 295 300	
cac gag gtc cca gca aag tct gat gtt tac tgt gag gtg tgt gaa ttc	960
His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe	
305 310 315 320	
ctg gtg aag gag gtg acc aag ctg att gac aac aac aag act gag aaa	1008
Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys	
325 330 335	
gaa ata ctc gac gct ttt gac aaa atg tgc tcg aag ctg ccg aag tcc	1056
Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser	
340 345 350	
ctg tcg gaa gag tgc cag gag gtg gtg gac acg tac ggc agc tcc atc	1104
Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile	
355 360 365	
ctg tcc atc ctg ctg gag gag gtc agc cct gag ctg gtg tgc agc atg	1152
Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met	
370 375 380	
ctg cac ctc tgc tct ggc acg cgg ctg cct gca ctg acc gtt cac gtg	1200
Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val	
385 390 395 400	
act cag cca aag gac ggt ggc ttc tgc gaa gtg tgc aag aag ctg gtg	1248
Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val	

405	410	415	
ggt tat ttg gat cgc aac ctg gag aaa aac agc acc aag cag gag atc			1296
Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile			
420	425	430	
ctg gct gct ctt gag aaa ggc tgc agc ttc ctg cca gac cct tac cag			1344
Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln			
435	440	445	
aag cag tgt gat cag ttt gtg gca gag tac gag ccc gtg ctg atc gag			1392
Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu			
450	455	460	
atc ctg gtg gag gtg atg gat cct tcc ttc gtg tgc ttg aaa att gga			1440
Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly			
465	470	475	480
gcc tgc ccc tcg gcc cat aag ccc ttg ttg gga act gag aag tgt ata			1488
Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile			
485	490	495	
tgg ggc cca agc tac tgg tgc cag aac aca gag aca gca gcc cag tgc			1536
Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys			
500	505	510	
aat gct gtc gag cat tgc aaa cgc cat gtg tgg aac taggaggagg			1582
Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn			
515	520		
aatattccat cttggcagaa accacagcat tggttttttt ctacttgtgt gtctggggga			1642
atgaacgcac agatctgttt gactttgtta taaaaatagg gctccccac ctccccatt			1702
tctgtgtcct ttattgtage attgctgtct gcaagggagc ccctagcccc tggcagacat			1762
agctgcttca gtgccccctt tctctctgct agatggatgt tgatgcactg gaggtctttt			1822
agcctgccct tgcattggcgc ctgctggagg aggagagagc tctgctggca tgagccacag			1882
tttcttgact ggaggccatc aaccctcttg gttgaggcct tgttctggcc ctgacatgtg			1942
cttgggcact ggtgggcctg ggcttctgag gtggcctcct gccctgatca gggaccctcc			2002
ccgctttcct gggcctctca gttgaacaaa gcagcaaac aaaggcagtt ttatatgaaa			2062
gattagaagc ctggaataat caggcttttt aaatgatgta attcccactg taatagcata			2122
gggatttttg aagcagctgc tgggtggcttg ggacatcagt ggggccaagg gttctctgtc			2182
cctggttcaa ctgtgatttg gctttcccggt gtctttcctg gtgatgcctt gtttgggggt			2242
ctgtggggtt ggggtgggaag agggcaatct gcctgaatgt aacctgctag ctctccgaag			2302

gccctgcggg cctggcttgt gtgagcgtgt ggacagtggg ggccgcgctg tgccctgctcg 2362  
 tgttgccctac atgtccctgg ctgttgaggc gctgcttcag cctgcacccc tcccttgtct 2422  
 catagatgct ccttttgacc ttttcaaata aatatggatg gcgagctcct aggcctctgg 2482  
 cttcctggta gagggcggca tgccgaaggg tctgctcggg gtggattgga tgctgggggtg 2542  
 tggggggttg aagctgtctg tggcccactt gggcacactt gggcacccac gcttctgtcc 2602  
 acttctgggtt gccaggagac agcaagcaaa gccagcagga catgaagttg ctattaaatg 2662  
 gacttcgtga tttttgtttt gcactaaagt ttctgtgatt taacaataaa attctgttag 2722  
 ccagaaaaaa aaaaaaaaaa aaaaaaa 2749

<210> 23  
 <211> 524  
 <212> PRT  
 <213> Homo sapiens

<400> 23  
 Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala  
 1 5 10 15  
 Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp  
 20 25 30  
 Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys  
 35 40 45  
 Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp  
 50 55 60  
 Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn  
 65 70 75 80  
 Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp  
 85 90 95  
 Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser  
 100 105 110  
 Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro  
 115 120 125  
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His  
 130 135 140  
 Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro  
 145 150 155 160

Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro  
 165 170 175

Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys  
 180 185 190

Asp Asn Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile  
 195 200 205

Gln Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu  
 210 215 220

His Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile  
 225 230 235 240

Cys Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met  
 245 250 255

Met His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp  
 260 265 270

Glu Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala  
 275 280 285

Ser Lys Asn Val Ile Pro Ala Leu Glu Leu Val Glu Pro Ile Lys Lys  
 290 295 300

His Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe  
 305 310 315 320

Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys  
 325 330 335

Glu Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser  
 340 345 350

Leu Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile  
 355 360 365

Leu Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met  
 370 375 380

Leu His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val  
 385 390 395 400

Thr Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val  
 405 410 415

Gly Tyr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile  
 420 425 430

Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln

435                      440                      445  
 Lys Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu  
     450                      455                      460  
 Ile Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly  
     465                      470                      475                      480  
 Ala Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile  
                     485                      490                      495  
 Trp Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys  
                     500                      505                      510  
 Asn Ala Val Glu His Cys Lys Arg His Val Trp Asn  
                     515                      520

<210> 24  
 <211> 80  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificial  
           Peptide Sequence

<400> 24  
 Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr  
     1                      5                      10                      15  
 Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe  
                     20                      25                      30  
 Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln  
                     35                      40                      45  
 Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu  
                     50                      55                      60  
 Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly  
                     65                      70                      75                      80

<210> 25  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>

C1  
conclude

<223> Description of Artificial Sequence: Artificial  
Peptide Sequence

<220>

<221> PEPTIDE

<222> (1)..(12)

<223> X at position 3, 11 and 12 is any amino acid; X at  
position 6 is any amino acid, but not L or R; X at  
position 8 and 10 is a charged amino acid; and X  
at position 9, when present is a charged residue

<400> 25

Leu Ile Xaa Asn Asn Xaa Thr Xaa Xaa Xaa Xaa Xaa

1

5

10